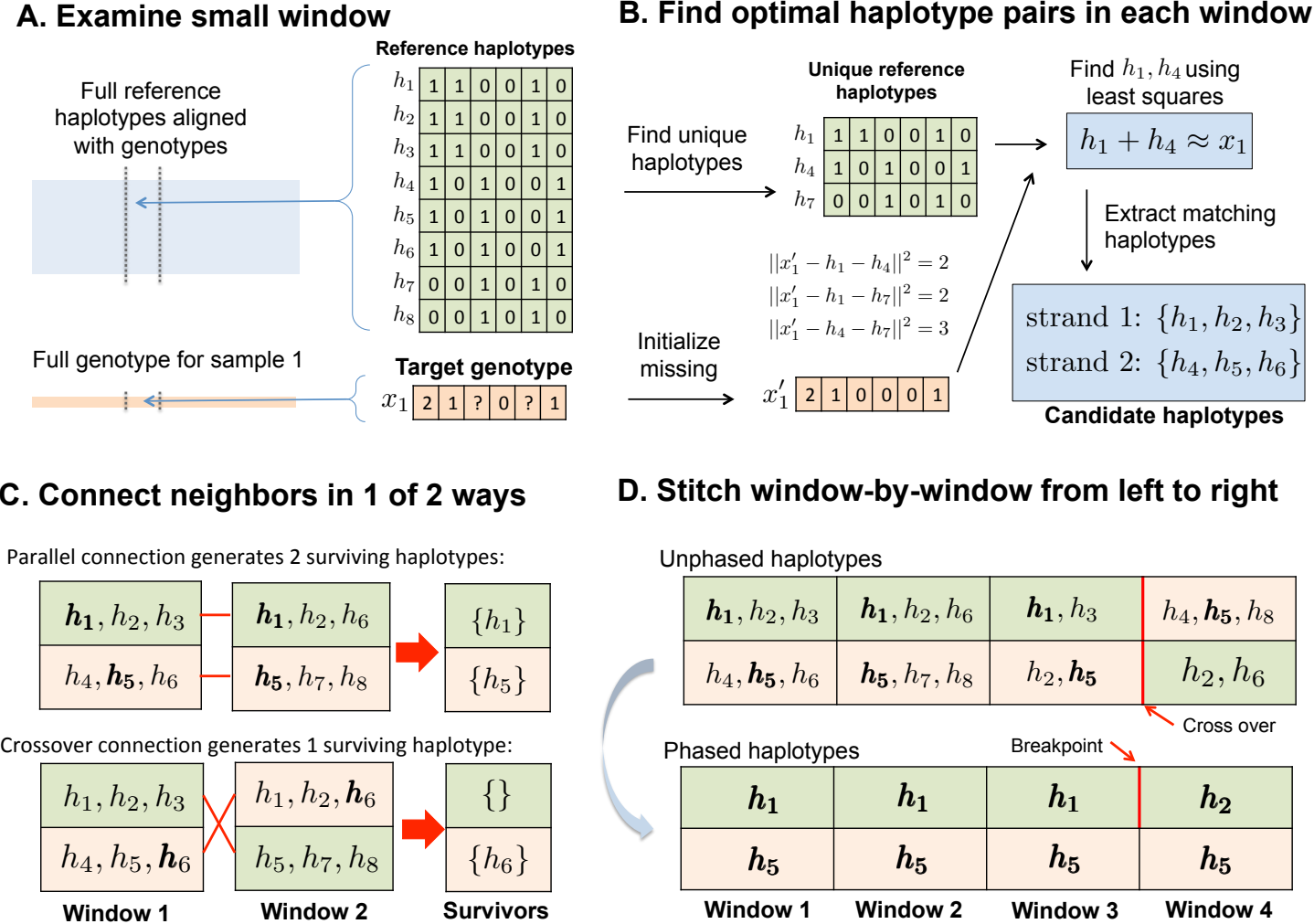
A. Examine small window
Reference haplotypes
Full reference haplotypes aligned with genotypes
Full genotype for sample 1
Target genotype
B. Find optimal haplotype pairs in each window
Unique reference haplotypes
Find unique haplotypes
Find h_1, h_4 using least squares
$h_1 + h_4 \approx x_1$
Extract matching haplotypes
$||x'_1 - h_1 - h_4||^2 = 2$
$||x'_1 - h_1 - h_7||^2 = 2$
$||x'_1 - h_4 - h_7||^2 = 3$
Initialize missing
strand 1: $\{h_1, h_2, h_3\}$
strand 2: $\{h_4, h_5, h_6\}$
Candidate haplotypes
C. Connect neighbors in 1 of 2 ways
Parallel connection generates 2 surviving haplotypes:
Crossover connection generates 1 surviving haplotype:
Window 1
Window 2
Survivors
D. Stitch window-by-window from left to right
Unphased haplotypes
Cross over
Phased haplotypes
Breakpoint
Window 1
Window 2
Window 3
Window 4